RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: *10/510,386*
Source: *PCT*
Date Processed by STIC: *10-19-04*

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/510,386_ : CRF Edit Date: _10-19-04_
Edited by: _RC_

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

_____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

__✓__ Deleted: __✓__ invalid beginning/end-of-file text ; ____ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_____ Other:

_____
_____
_____

`PCT

```
 3 <110> APPLICANT: Andersen, Jens Tonne
 4        Clausen, Ib Groth
 5        Jorgensen, Steen Troels
 6        Olsen, Peter Bjarke
 7        Rasmussen, Michael Dolberg
 9 <120> TITLE OF INVENTION: Improved Bacillus Host Cell
11 <130> FILE REFERENCE: 10294.204-US
13 <140> CURRENT APPLICATION NUMBER: US/10/510,386
13 <141> CURRENT FILING DATE: 2004-10-04
13 <160> NUMBER OF SEQ ID NOS: 248
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3405
19 <212> TYPE: DNA
20 <213> ORGANISM: Bacillus licheniformis
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (501)..(2906)
27 <400> SEQUENCE: 1
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30 tattaaactt tcttgctcta tcttatccca gcaaaatgaa aatgtttgtc acaatgtgtg   120
32 tgcaaaatga ttctagtttt tagaagtttt gttgaaaact gaaggaatcg catgattcag   180
34 cggatacaaa ccatgaatgt aacttactca cagcttatcc taaggataaa cacatattac   240
36 ccacaggata tatccacata tccacatact tattcaatat ttagtataag aacgtatatt   300
38 ccctacaata tctatacaca agtttattca cttatacaca gtaaattgtg cataaatcta   360
40 gagaaattca ctccaataca ttgaatcttt gaaaattatt tctatatata gaaggatttt   420
42 tttgaaactg agagaatatt ttaaaagttc gaaactctaa taattacaaa gaaacattta   480
44 tccagaaggg ggaaaacaga ttg aga aaa agt atc gtg cgc tat ttt gtt atg   533
45                         Leu Arg Lys Ser Ile Val Arg Tyr Phe Val Met
46                          1               5                  10
48 gct ttt att cta tta ttt gcg tta tcc aca ttc ctc acc gga gtg cag     581
49 Ala Phe Ile Leu Leu Phe Ala Leu Ser Thr Phe Leu Thr Gly Val Gln
50              15                  20                  25
52 gca act tcc gtt ccc gat aaa aag tcg cct gag ctt gag aaa gct gaa     629
53 Ala Thr Ser Val Pro Asp Lys Lys Ser Pro Glu Leu Glu Lys Ala Glu
54          30                  35                  40
56 atc tac ggt gat att gat gtg acg tct gat aaa cag acg acg gtt atc     677
57 Ile Tyr Gly Asp Ile Asp Val Thr Ser Asp Lys Gln Thr Thr Val Ile
58      45                  50                  55
60 gtg gaa ctg aaa gaa aag tcg ctt gcc gaa gca aaa gcg gac gga gaa     725
61 Val Glu Leu Lys Glu Lys Ser Leu Ala Glu Ala Lys Ala Asp Gly Glu
62 60                  65                  70                  75
64 aaa caa acg aag gct tct cta aaa aca gct cga agc aaa gcg ctg aaa     773
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65 Lys Gln Thr Lys Ala Ser Leu Lys Thr Ala Arg Ser Lys Ala Leu Lys
66             80               85               90
68 aca ctt aaa aaa gcg aaa gta aac cgc gaa tac gac cgt gta ttt tcg      821
69 Thr Leu Lys Lys Ala Lys Val Asn Arg Glu Tyr Asp Arg Val Phe Ser
70             95               100              105
72 ggc ttt tct atg aaa ctg ccg gcc agt gaa att cca aag ctg ctc gcc      869
73 Gly Phe Ser Met Lys Leu Pro Ala Ser Glu Ile Pro Lys Leu Leu Ala
74             110              115              120
76 gtc aag gaa gtt aaa gcg gtt tat cca aac gca act tac aaa cct gac      917
77 Val Lys Glu Val Lys Ala Val Tyr Pro Asn Ala Thr Tyr Lys Pro Asp
78     125              130              135
80 agc gta aaa gga aaa gac gtg aca ctt gca gca gac gcc att tat cca      965
81 Ser Val Lys Gly Lys Asp Val Thr Leu Ala Ala Asp Ala Ile Tyr Pro
82 140             145              150                  ·155
84 cag atg gat aaa agt gcc ccg ttc atc gga gcg gat cag gca tgg aaa     1013
85 Gln Met Asp Lys Ser Ala Pro Phe Ile Gly Ala Asp Gln Ala Trp Lys
86             160              165              170
88 tcg ggc tat acc ggt aaa ggc att aag gta gcc gtt att gat acg ggc     1061
89 Ser Gly Tyr Thr Gly Lys Gly Ile Lys Val Ala Val Ile Asp Thr Gly
90             175              180              185
92 gtg gat tac acc cat ccc gac tta aag aat aat ttc ggc cca tat aag     1109
93 Val Asp Tyr Thr His Pro Asp Leu Lys Asn Asn Phe Gly Pro Tyr Lys
94             190              195              200
96 ggc tat gac ttt gtg gat aat gat tat gat cca cag gaa aca ccg aca     1157
97 Gly Tyr Asp Phe Val Asp Asn Asp Tyr Asp Pro Gln Glu Thr Pro Thr
98     205              210              215
100 ggc gac ccg cgc ggc gga gcg act gat cac ggc act cat gtt gca gga    1205
101 Gly Asp Pro Arg Gly Gly Ala Thr Asp His Gly Thr His Val Ala Gly
102 220             225              230                  235
104 aca atc gcc gcg aac gga cag att aaa ggc gtg·gcg cct gaa gca acg    1253
105 Thr Ile Ala Ala Asn Gly Gln Ile Lys Gly Val Ala Pro Glu Ala Thr
106             240              245              250
108 ctt ctt gct tac cgc gtg ctc ggc ccc ggc ggc tca ggc aca acc gag    1301
109 Leu Leu Ala Tyr Arg Val Leu Gly Pro Gly Gly Ser Gly Thr Thr Glu
110             255              260              265
112 aat gtg att gcg ggc att gaa aaa gcc gtt gca gac gga gca aaa gtg    1349
113 Asn Val Ile Ala Gly Ile Glu Lys Ala Val'Ala Asp Gly Ala Lys·Val
114             270              275              280
116 atg aac ctc tca ttg gga aat tcg ctg aac agc cct gat tat gca aca    1397
117 Met Asn Leu Ser Leu Gly Asn Ser Leu Asn Ser Pro Asp Tyr Ala Thr
118     285              290              295
120 agc atc gca ctg gac tgg gcg atg gct gaa ggg gtt gtc gcc gtt acg    1445
121 Ser Ile Ala Leu Asp Trp Ala Met Ala Glu Gly Val Val Ala Val Thr
122 300             305              310                  315
124 tca aac ggt aac agc gga·ccg gaa aac tgg acg gtc ggc tcg ccg gga    1493
125 Ser Asn Gly Asn Ser Gly Pro Glu Asn Trp Thr Val Gly Ser Pro Gly
126                 .320              325              330.
128 aca tca agg gtt gcg att tcc gtc ggc gca tca cag ctt ccg tat aat    1541
129 Thr Ser Arg Val Ala Ile Ser Val Gly Ala Ser Gln Leu Pro Tyr Asn
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130               335                 340                 345
132 gag tat tcg gtg acg ctt cct tcg tat tca tca gca aag gtg atg gga    1589
133 Glu Tyr Ser Val Thr Leu Pro Ser Tyr Ser Ser Ala Lys Val Met Gly
134         350                 355                 360
136 tac caa gag gaa aag gat ctt gaa gca ttg aac ggt caa gag gtg gaa    1637
137 Tyr Gln Glu Glu Lys Asp Leu Glu Ala Leu Asn Gly Gln Glu Val Glu
138         365                 370                 375
140 ctc gtt gaa gcc ggc ctc gga caa gct gac gat ttc tca ggc aaa gat    1685
141 Leu Val Glu Ala Gly Leu Gly Gln Ala Asp Asp Phe Ser Gly Lys Asp
142 380                 385                 390                 395
144 gtg aaa gga aaa gtt gcg gtt atc cag aga ggc gtc ata cca ttt gtt    1733
145 Val Lys Gly Lys Val Ala Val Ile Gln Arg Gly Val Ile Pro Phe Val
146                 400                 405                 410
148 gat aag gct gaa aat gcc aaa aac gcc ggc gct atc gga gcc gtg att    1781
149 Asp Lys Ala Glu Asn Ala Lys Asn Ala Gly Ala Ile Gly Ala Val Ile
150                 415                 420                 425
152 tac aat aat gca aca ggg gaa atc gag gca aac gtc atg ggg atg gcc    1829
153 Tyr Asn Asn Ala Thr Gly Glu Ile Glu Ala Asn Val Met Gly Met Ala
154         430                 435                 440
156 gta ccg acc gtc aaa ttg tca aaa gaa gag ggc gaa aag ctt gtt caa    1877
157 Val Pro Thr Val Lys Leu Ser Lys Glu Glu Gly Glu Lys Leu Val Gln
158         445                 450                 455
160 cag atc aaa gaa ggg aaa cac tcc gtt gtc ttt tct ttc aaa ttg gac    1925
161 Gln Ile Lys Glu Gly Lys His Ser Val Val Phe Ser Phe Lys Leu Asp
162 460                 465                 470                 475
164 aaa aag ctg ggg gaa aca att gcc tca ttc tcg tcc cgc ggg cct gtc    1973
165 Lys Lys Leu Gly Glu Thr Ile Ala Ser Phe Ser Ser Arg Gly Pro Val
166                 480                 485                 490
168 atg gat aca tgg atg att aaa cct gac gtt tca gcg cca ggc gtc aac    2021
169 Met Asp Thr Trp Met Ile Lys Pro Asp Val Ser Ala Pro Gly Val Asn
170                 495                 500                 505
172 atc gtc agc acc att ccg acc cac gat ccg aaa aac ccg tac ggt tac    2069
173 Ile Val Ser Thr Ile Pro Thr His Asp Pro Lys Asn Pro Tyr Gly Tyr
174         510                 515                 520
176 ggt tca aaa cag gga aca agc atg gct tcc ccg cat gtc gcg gga acg    2117
177 Gly Ser Lys Gln Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Thr
178         525                 530                 535
180 gca gcc ata tta aag cag gcc aaa ccg gat tgg acg cct gag caa atc    2165
181 Ala Ala Ile Leu Lys Gln Ala Lys Pro Asp Trp Thr Pro Glu Gln Ile
182 540                 545                 550                 555
184 aaa ggc gta ctg atg aat acg gcg gaa aaa ctg acg gat gaa aat gga    2213
185 Lys Gly Val Leu Met Asn Thr Ala Glu Lys Leu Thr Asp Glu Asn Gly
186                 560                 565                 570
188 aag cct ctc cct cac aat acg caa gga gcg ggc agc atc cgc atc atg    2261
189 Lys Pro Leu Pro His Asn Thr Gln Gly Ala Gly Ser Ile Arg Ile Met
190         575                 580                 585
192 gag gcc ctt aaa gct tca tcc att gta acg ccg ggc agc cat tca tac    2309
193 Glu Ala Leu Lys Ala Ser Ser Ile Val Thr Pro Gly Ser His Ser Tyr
194         590                 595                 600
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196 gga aca ttc ctg aaa gac aaa ggg aaa cag acg aaa aaa caa gcg ttc    2357
197 Gly Thr Phe Leu Lys Asp Lys Gly Lys Gln Thr Lys Lys Gln Ala Phe
198     605             610             615
200 acg att gaa aac ctt tct tca cac aga aaa gcc tat cag ctc gaa tac    2405
201 Thr Ile Glu Asn Leu Ser Ser His Arg Lys Ala Tyr Gln Leu Glu Tyr
202 620             625             630             635
204 tcc ttt aaa gga acg ggc atc acg gta tca gga acg gaa cga gtc gtg    2453
205 Ser Phe Lys Gly Thr Gly Ile Thr Val Ser Gly Thr Glu Arg Val Val
206             640             645             650
208 gta ccg gcc aat caa aca ggt aaa gca gcg gca aaa gta acc gtc aat    2501
209 Val Pro Ala Asn Gln Thr Gly Lys Ala Ala Ala Lys Val Thr Val Asn
210             655             660             665
212 tcc gcg aaa acg aaa gca ggc aca tat gaa ggc acg gtt tac atc cgt    2549
213 Ser Ala Lys Thr Lys Ala Gly Thr Tyr Glu Gly Thr Val Tyr Ile Arg
214         670             675             680
216 gaa gac gga aga aaa gtc gcc gaa atc ccg ctc cta ttg atc gtc aaa    2597
217 Glu Asp Gly Arg Lys Val Ala Glu Ile Pro Leu Leu Leu Ile Val Lys
218     685             690             695
220 gag cca gac tac ccg cgc gtc aca tcc gta aca gtt gaa ccg gga gca    2645
221 Glu Pro Asp Tyr Pro Arg Val Thr Ser Val Thr Val Glu Pro Gly Ala
222 700             705             710             715
224 aag cag ggc gct tac acg atc gaa gcc tac ctg ccg ggc ggg gct gaa    2693
225 Lys Gln Gly Ala Tyr Thr Ile Glu Ala Tyr Leu Pro Gly Gly Ala Glu
226             720             725             730
228 gag ctc gca ttt ctc gtc tat gat gaa aac ctg aac ctt ctc ggc cag    2741
229 Glu Leu Ala Phe Leu Val Tyr Asp Glu Asn Leu Asn Leu Leu Gly Gln
230             735             740             745
232 gcc ggc gtt tac aaa aac cag ggc aaa ggc tat caa tct tat caa tgg    2789
233 Ala Gly Val Tyr Lys Asn Gln Gly Lys Gly Tyr Gln Ser Tyr Gln Trp
234             750             755             760
236 aac ggc aaa atc aat gac gcc gca tcc ctt aag tcc gga aaa tac tat    2837
237 Asn Gly Lys Ile Asn Asp Ala Ala Ser Leu Lys Ser Gly Lys Tyr Tyr
238     765             770             775
240 atg ctt gcc tat gca tcc gcc aaa ggg aaa tca agc tac gta ttg acg .  2885
241 Met Leu Ala Tyr Ala Ser Ala Lys Gly Lys Ser Ser Tyr Val Leu Thr
242 780             785             790             795
244 gaa gac cct ttt atc gtc gaa taatgacaag ccttgttgag aaccactcaa       2936
245 Glu Asp Pro Phe Ile Val Glu
246             800
248 caaggctttt ttatgttaaa atacggataa tgcgttcagg agaagctccc ccttctcttc  2996
250 aaaacgtgaa aaaagcaatc ggaggacatc gtgtatatgc tttctttat cgtattattc   3056
252 ggcttatcct tcattattgt ctgctttata tttttcacga ttttgtactt cgccgtcaac  3116
254 ctgcagaagc gcgagcccaa gccttttcaa aaagctgcgg agcaaaccgt cgataccatc  3176
256 atcctcattc cgatcagctg ctgtttacc gctttataca tatgcattct gtttattctt   3236
258 ttcccaatcc gccatttct cgattttttt cagcaaaaac gctaaattga ctgatgaaac   3296
260 gcttcggcca gcagccggta tgaatccaat ctgtcttgaa aatcgtgggt gatcgtcacc  3356
262 gccatgattt cgtccgttcc gtaagcgccg gccagttcaa gcagctgtt             3405
265 <210> SEQ ID NO: 2
266 <211> LENGTH: 802
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RAW SEQUENCE LISTING   DATE: 10/19/2004
PATENT APPLICATION: US/10/510,386   TIME: 17:14:43

Input Set : N:\KEISHA\10510386.txt
Output Set: N:\CRF4\10192004\J510386.raw

267 <212> TYPE: PRT
268 <213> ORGANISM: Bacillus licheniformis
270 <400> SEQUENCE: 2
272 Leu Arg Lys Ser Ile Val Arg Tyr Phe Val Met Ala Phe Ile Leu Leu
273 1   5   10   15
276 Phe Ala Leu Ser Thr Phe Leu Thr Gly Val Gln Ala Thr Ser Val Pro
277   20   25   30
280 Asp Lys Lys Ser Pro Glu Leu Glu Lys Ala Glu Ile Tyr Gly Asp Ile
281   35   40   45
284 Asp Val Thr Ser Asp Lys Gln Thr Thr Val Ile Val Glu Leu Lys Glu
285   50   55   60
288 Lys Ser Leu Ala Glu Ala Lys Ala Asp Gly Glu Lys Gln Thr Lys Ala
289 65   70   75   80
292 Ser Leu Lys Thr Ala Arg Ser Lys Ala Leu Lys Thr Leu Lys Lys Ala
293   85   90   95
296 Lys Val Asn Arg Glu Tyr Asp Arg Val Phe Ser Gly Phe Ser Met Lys
297   100   105   110
300 Leu Pro Ala Ser Glu Ile Pro Lys Leu Leu Ala Val Lys Glu Val Lys
301   115   120   125
304 Ala Val Tyr Pro Asn Ala Thr Tyr Lys Pro Asp Ser Val Lys Gly Lys
305   130   135   140
308 Asp Val Thr Leu Ala Ala Asp Ala Ile Tyr Pro Gln Met Asp Lys Ser
309 145   150   155   160
312 Ala Pro Phe Ile Gly Ala Asp Gln Ala Trp Lys Ser Gly Tyr Thr Gly
313   165   170   175
316 Lys Gly Ile Lys Val Ala Val Ile Asp Thr Gly Val Asp Tyr Thr His
317   180   185   190
320 Pro Asp Leu Lys Asn Asn Phe Gly Pro Tyr Lys Gly Tyr Asp Phe Val
321   195   200   205
324 Asp Asn Asp Tyr Asp Pro Gln Glu Thr Pro Thr Gly Asp Pro Arg Gly
325   210   215   220
328 Gly Ala Thr Asp His Gly Thr His Val Ala Gly Thr Ile Ala Ala Asn
329 225   230   235   240
332 Gly Gln Ile Lys Gly Val Ala Pro Glu Ala Thr Leu Leu Ala Tyr Arg
333   245   250   255
336 Val Leu Gly Pro Gly Gly Ser Gly Thr Thr Glu Asn Val Ile Ala Gly
337   260   265   270
340 Ile Glu Lys Ala Val Ala Asp Gly Ala Lys Val Met Asn Leu Ser Leu
341   275   280   285
344 Gly Asn Ser Leu Asn Ser Pro Asp Tyr Ala Thr Ser Ile Ala Leu Asp
345   290   295   300
348 Trp Ala Met Ala Glu Gly Val Val Ala Val Thr Ser Asn Gly Asn Ser
349 305   310   315   320
352 Gly Pro Glu Asn Trp Thr Val Gly Ser Pro Gly Thr Ser Arg Val Ala
353   325   330   335
356 Ile Ser Val Gly Ala Ser Gln Leu Pro Tyr Asn Glu Tyr Ser Val Thr
357   340   345   350
360 Leu Pro Ser Tyr Ser Ser Ala Lys Val Met Gly Tyr Gln Glu Glu Lys
361   355   360   365

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/19/2004
PATENT APPLICATION: US/10/510,386   TIME: 17:14:44

Input Set : **N:\KEISHA\10510386.txt**
Output Set: **N:\CRF4\10192004\J510386.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:205; N Pos. 255,257

VERIFICATION SUMMARY   DATE: 10/19/2004
PATENT APPLICATION: **US/10/510,386**   TIME: 17:14:44

Input Set : **N:\KEISHA\10510386.txt**
Output Set: **N:\CRF4\10192004\J510386.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:21840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:240